

1 GAT TTT TTG TGA TAT CTT CGG GGG GGG GAA CCT ATT GTA TAA ACG CCA ACC AAC CGG
64 CCC TTT TTT GGG TAC CTG GCC ATT TTA CTT GGC CCA TTT TGG TAA AAT GTT CCT TTC CCT GCG
127 TTA ATC CCC CTG ATT CCT TGT GGG ATA ACC CGT ATT CCC CCC CTT AGA GTG ATT TTG AAA ACC
190 CTT TCG CCC GGA AGG GGA CCG ACC GAG CCC AGC GAT TCA TGG AGC GAG GAA AGC GGG AAG AGC
253 GCC CAA TAC CCA AGC CGC CTC TCG CCG CGT TGT GCG ATT CAT TAA TAC AGC TGC CAC GAC
316 AGG TTT CCC GAC TGG AAA GCG GTC AGT GAG CGC AAC ACA ATT AAT GTG AGT TAG CTC ACT CAT
379 TAG GCA CCC CAG GCT TTA CAC TTT ATG CTT CGT GCT CGT ATG TTG TGT GGA ATT GTG AGC GGA
442 TAA CAA TTT CAC ACA GGA AAC AGC TAT GAC CAT GAT TAC GTC CAA GCT CGA AAT TAA CCC TCA
505 CTA AAG GGA ACA AAA ACT GGA GCT CCA CGG TGG CGG CCG CTC TAG AAC TAG TGG ATC CCC
568 CGG GCT CCA GGA ATT CGC CAC GAC CGG GAG CGA GGA GCC GCC AGA CTA CGG GCG A ATG
629 GCG ACC CGC AGC CCT GGC GTC GTG ATT ATG GAT GAT TGG CCA GGG TAT GAC TGT AAT TTA TTC
Ala Thr Arg Ser Pro Gly Val Ile Met Asp Asp Trp Pro Gly Tyr Asp Leu Asn Leu Phe

FIG. 1A

FIG. 1B

692	ACG	TAC	CCA	CAG	CAC	TAT	GGA	GAC	TTC	GAG	TAT	GTC	CTC	ATC	CCT	CAT	GGT	ATC	ATT	GTG		
Thr	Tyr	Pro	Gln	His	Tyr	Tyr	Gly	Asp	Leu	Glu	Tyr	Val	Leu	Ile	Pro	His	Gly	Ile	Ile	Val		
755	GAC	AGA	ATT	GAG	CGG	CTG	GCC	AAG	GAT	ATT	ATG	AAA	GAC	ATA	GGA	TAT	AGT	GAC	ATC	ATG	GTC	
Asp	Arg	Ile	Glu	Arg	Leu	Ala	Lys	Asp	Ile	MET	Lys	Asp	Ile	Gly	Tyr	Ser	Asp	Ile	MET	Val		
818	CTG	TGT	GTG	CTT	AAA	GGG	GGG	TAC	AAA	TTC	TGT	GCT	GAT	CTC	GTA	GAA	CAC	CCT	AAG	AAC	ATC	
Leu	Cys	Val	Leu	Lys	Gly	Gly	Gly	Tyr	Lys	Phe	Cys	Ala	Asp	Leu	Val	Glu	His	Leu	Lys	Asn	Ile	
881	AGC	CGA	AAT	TCA	GAT	CGG	TTT	GTC	TCA	ATG	AAG	GTT	GAT	TTC	ATC	AGA	CTA	AAA	AGT	TAC	AGG	
Ser	Arg	Asn	Ser	Asp	Arg	Phe	Val	Ser	MET	Lys	Val	Asp	Phe	Ile	Arg	Leu	Lys	Ser	Tyr	Arg		
944	AAT	GAC	CAG	TCC	ATG	GGT	GAG	ATG	CAG	ATA	ATC	GGA	GGC	GGT	GAT	CTT	TCA	ACG	CTG	GCT	GGA	
Asn	Asp	Gln	Ser	MET	Gly	Glu	MET	Gln	Ile	Ile	Gly	Gly	Gly	Asp	Ile	Arg	Leu	Ser	Thr	Leu	Ala	Gly
1007	AAG	AAT	TTT	CTC	ATT	GTT	GAG	GAT	GTT	GTC	GGA	ACT	GGG	AGG	ACC	ATG	AAA	GCA	CTA	CTC	AGC	
Lys	Asn	Phe	Ile	Val	Glu	Asp	Val	Val	Gly	Thr	Gly	Arg	Thr	MET	Lys	Ala	Leu	Leu	Leu	Ser		
1070	AAT	ATA	GAG	AAA	TAC	AAG	CCC	AAC	ATG	ATT	AAG	GTA	GCC	AGT	TTG	TTG	GAG	AGA	ACA	TCC		
Asn	Ile	Glu	Lys	Tyr	Lys	Pro	Asn	MET	Ile	Lys	Val	Ala	Ser	Leu	Leu	Val	Lys	Arg	Thr	Ser		
1133	AGA	AGT	GAC	GGC	TTT	AGA	CCT	GAC	TAT	GCT	GGA	TTT	GAG	ATT	CCA	CAC	TAA	TTT	GTG	GTG	GGA	
Arg	Ser	Asp	Gly	Gly	Phe	Arg	Pro	Asp	Tyr	Ala	Gly	Phe	Glu	Ile	Pro	His	Leu	Phe	Val	Val	Gly	

FIG. 1C

1196 TAT GCC TTA GAT TAC AAT GAA TAC TTC AGA GAT CTG AAT CAC ATA TGC GTC ATC AAT GAG CAC
Tyr Ala Leu Asp Tyr Asn Glu Tyr Asn Glu Tyr Phe Arg Asp Leu Asn His Ile Cys Val Ile Asn Glu His
1259 GGG TAA AGG AAA ATA TCG AGT CTT AAA GAC ATG AAT TCT CAC CAC TAA AGG CCC CAG ATA GGA
Gly STP

1322 TCA TTT TTA CGC CTG TCT TGG GGA GCC AGT TGC AAG TTG GGC CCC CCC GGA TCT TCA TCA GGA

1385 GG

1 MATRSPGVVISDDEPGYDLDLFCIPNHYAEDLERVFIPHGLIMDRTERLARDVMKE 56
1 ||||||| |||| ||||:||..|| :||| :|||:|||:|||:|||:|||:
1 MATRSPGVVIMDDWPGYDLNLFTYPQHYYGDLEYVLIPHGIIVDRIERLAKDIMKD 56
57 MGGHHIVALCVLKGGYKFFADLLDYIKALNRNSDRSIPMTVDFIRLKSYCNDQSTG 112
:| .|.:||||| ||||:|..| ||| :.|||:|||:|||:|||:
57 IGYS DIMVLCVLKGGYKFCADLVEHLKNISRNSDRFVSMKVDFIRLKSYRNDQSMG 112
113 DIKVIGGDDLSTLTGKNVLIVEDIIDTGKTMQTLLSLVRQYNPKMVKVASLLVKRT 168
:::|||:|||..|||.||||:|||:|||:|||:|||:|||:|||:
113 EMQIIGGGDLSTLAGKNFLIVEDVVGTGRTMKALLSIEKYKPNMIKVASLLVKRT 168
169 PRSVGYPDFVGFEIPDKFVVGYALDYNEYFRDLNHVCVISETGKAKYKA 218
.|| |:|||:|||..|||:|||:|||:|||:|||:|||:|||:
169 SRSDGFRPDYAGFEIPHLFVVGYALDYNEYFRDLNHICVINEHG*RKISS 218

FIG.2

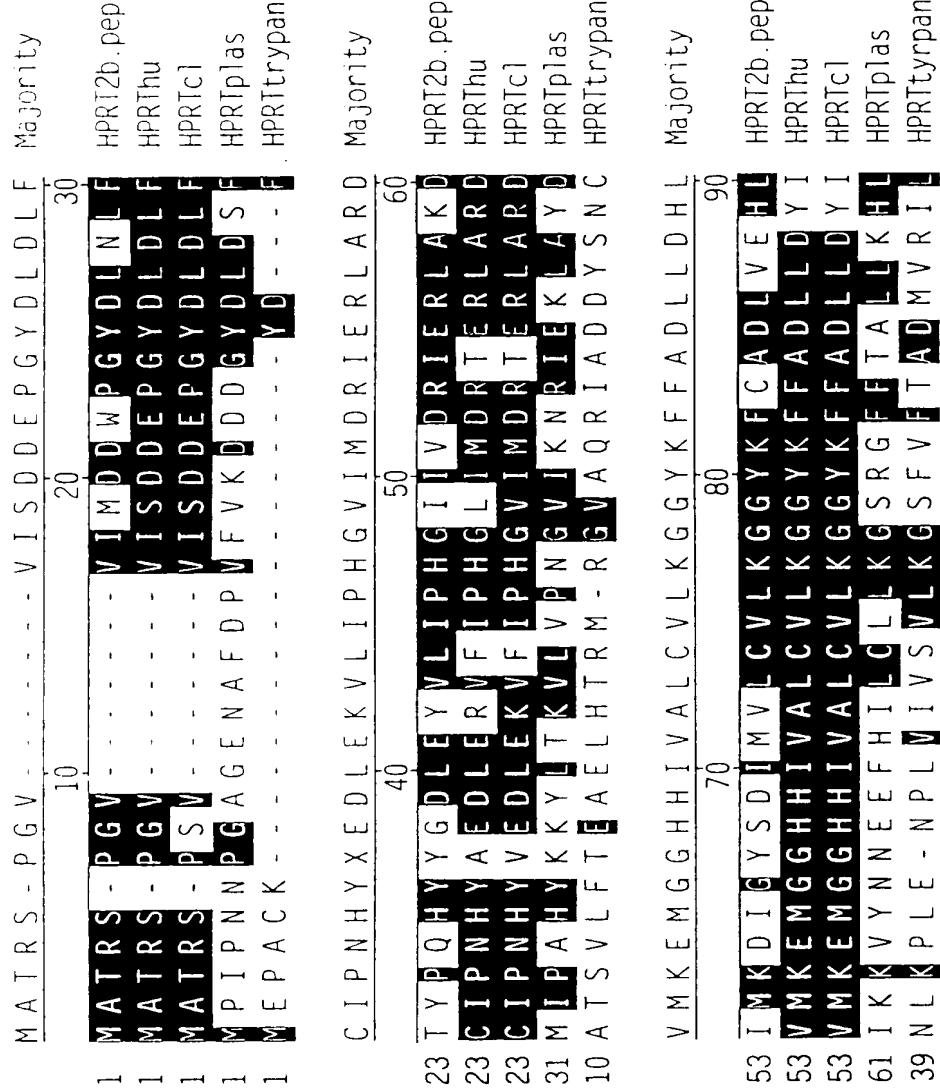


FIG. 3A

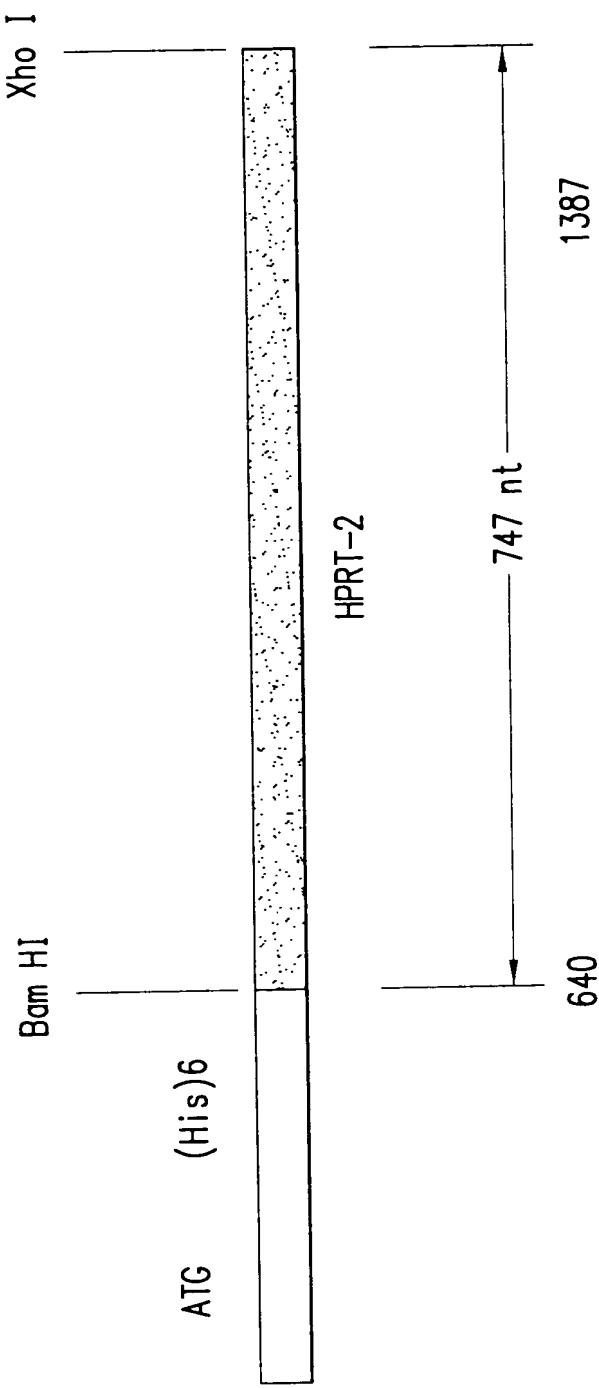
K A L N R N S D R S V P M T V	- - -	D F I R L K S Y C N D Q	Majority
100			
K N I S R N S D R F V S M K V	- - -	D F I R L K S Y R N D Q	HPRT2b.pep
83 K A L N R N S D R S I P M T V	- - -	D F I R L K S Y C N D Q	HPRTThu
83 K A L N R N S D R S I P M T V	- - -	D F I R L K S Y C N D Q	HPRTC1
S R I H N Y S A V E M S K P L F G E H Y V R V K S Y C N D Q	-	D F I R L K S Y C N D Q	HPRTplas
G D F G - - - V P T R V	- - -	E F L R A S S Y G H D T	HPRTtrypan
110			
S T G D I K V I G G D D L S T L T G K N V L I V E D I I D T	Majority		
120			
S M G E M Q I I G G G D L S T L A G K N F L I V E D V V G I	Majority		
110 S T G D I K V I G G D D L S T L T G K N V L I V E D I I D T	HPRT2b.pep		
110 S T G D I K V I G G D D L S T L T G K N V L I V E D I I D T	HPRTThu		
110 S T G D I K V I G G D D L S T L T G K N V L I V E D I I D T	HPRTC1		
121 S T G T L E I V S - E D L S C L K G K H V L I V E D I I D T	HPRTplas		
89 K S C G R V D V K A D G L C D I R G K H V L V L E D I I D T	HPRTtrypan		
130			
S T G D I K V I G G D D L S T L T G K N V L I V E D I I D T	Majority		
140			
G K T M Q T L L S L V K K Y E P K M V K V A S L L V K R T S	Majority		
150			
140 G R T M K A L L S N I E K Y K P N M I K V A S L L V K R T S	Majority		
140 G K T M Q T L L S L V R Q Y N P K M V K V A S L L V K R T P	HPRT2b.pep		
140 G K T M Q T L L S L V K R Y N P K M V K V A S L L V K R T S	HPRTThu		
140 G K T L V K F C E Y L K K F E I K T V A I A C L F I K R T P	HPRTC1		
150 G K T L V D S L K K S E P A S I K T L V A I D K P G G	HPRTplas		
119 A L I L R E V V D S L K K S E P A S I K T L V A I D K P G G	HPRTtrypan		
160			
G K T M Q T L L S L V K K Y E P K M V K V A S L L V K R T S	Majority		
170			
140 G R T M K A L L S N I E K Y K P N M I K V A S L L V K R T S	Majority		
140 G K T M Q T L L S L V R Q Y N P K M V K V A S L L V K R T P	HPRT2b.pep		
140 G K T M Q T L L S L V K R Y N P K M V K V A S L L V K R T S	HPRTThu		
150 G K T L V K F C E Y L K K F E I K T V A I A C L F I K R T P	HPRTC1		
119 A L I L R E V V D S L K K S E P A S I K T L V A I D K P G G	HPRTplas		
180			

FIG. 3B

FIG. 3C

<p>R S V G F K P D F V G F E I P D K F V V G Y A L D Y N E Y F</p> <p>170 R S D G F R P D Y A G F E I P H L F V V G Y A L D Y N E Y F</p> <p>170 R S V G Y K P D F V G F E I P D K F V V G Y A L D Y N E Y F</p> <p>170 R S V G Y R P D F V G F E I P D K F V V G Y A L D Y N E Y F</p> <p>180 L W N G F K A D F V G F S I P D H F V V G Y S L D Y N E I F</p> <p>149 R K I P F T A E Y V V A D V P N V F V V G Y G L D Y D Q S Y</p>	<p>Majority</p> <p>190</p> <p>200</p> <p>210</p> <p>HPRT2b.pep</p> <p>HPRTThu</p> <p>HPRTC1</p> <p>HPRTplas</p> <p>HPRTtrypan</p>
<p>R D L N H V C V I S - - - - -</p> <p>200 R D L N H I C V I N - - - - -</p> <p>200 R D L N H V C V I S - - - - -</p> <p>200 R D L N H I C V I S - - - - -</p> <p>210 R D L D H C C L V N - - - - -</p> <p>179 R E V R O V V I L K P S V Y E T W G K E L E R R K A A G E A</p>	<p>Majority</p> <p>220</p> <p>230</p> <p>240</p> <p>HPRT2.pep</p> <p>HPRTThu</p> <p>HPRTC1</p> <p>HPRTplas</p> <p>HPRTtrypan</p>
<p>- - -</p> <p>212</p> <p>218</p> <p>218</p> <p>231 L</p> <p>209 K R</p>	<p>Majority</p>

FIG. 4



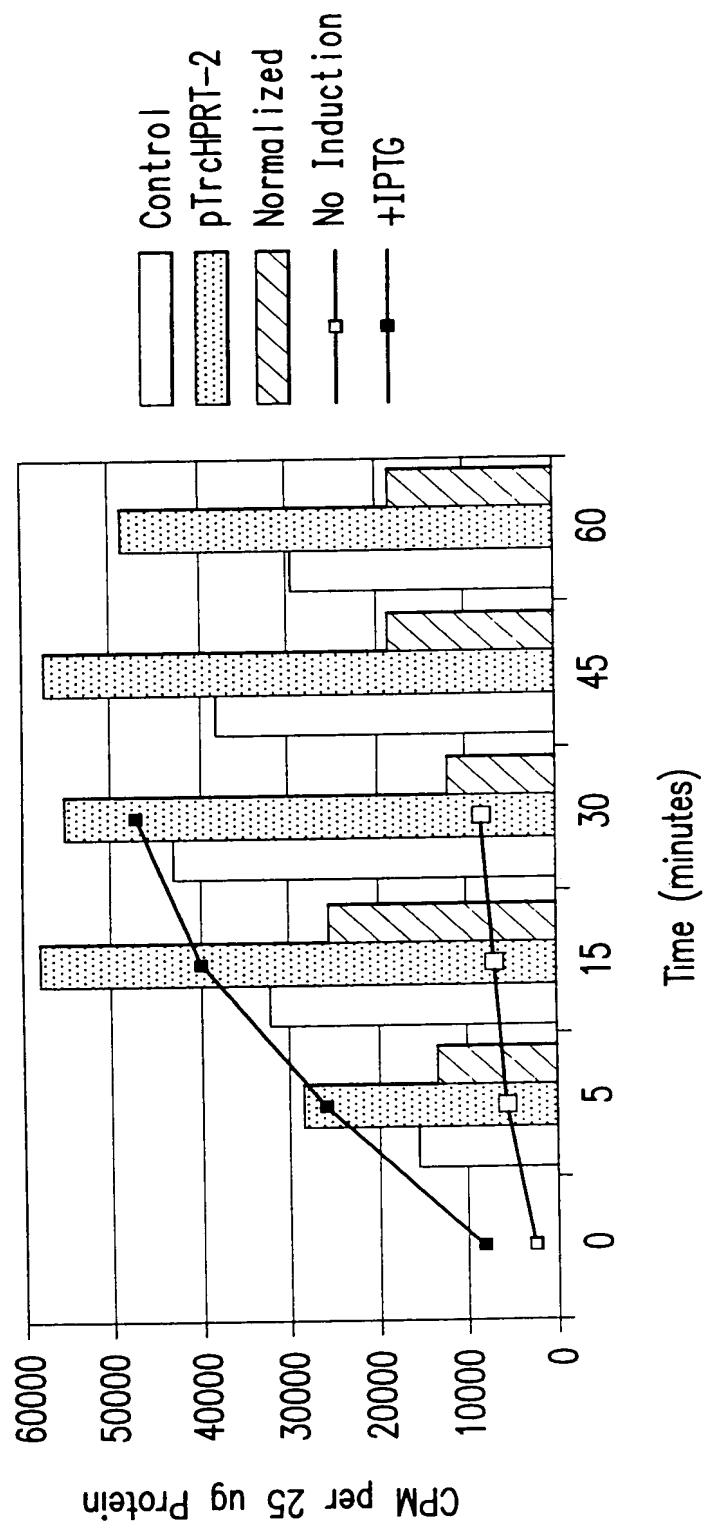


FIG. 5